



SEQUENCE LISTING

<110> Pausch, Mark H
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011

<141> 1997-03-11

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<151> 1994-10-31

<150> PCT/US95/14364

<151> 1995-10-25

<160> 67

<170> PatentIn Ver. 2.1

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<213> Drosophila melanogaster

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 420 425 430
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 435 440 445
 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
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 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
 465 470 475 480
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 485 490 495
 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
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 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
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 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
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 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
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 Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
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 35 40 45
 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
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330

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<400> 6

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<213> *Drosophila melanogaster*

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<213> *Drosophila melanogaster*

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 <213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<212> DNA
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<213> Drosophila melanogaster

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<210> 36
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 <212> DNA
 <213> *Caenorhabditis elegans*

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 <213> *Drosophila melanogaster*

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Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu	35	40	45
Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu	50	55	60
Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro	65	70	75
Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe	85	90	95
Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser	100	105	110
Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile	115	120	125
Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe	130	135	140
Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met	145	150	155
Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr	165	170	175
Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro	180	185	190
Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser	195	200	205
Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr	210	215	220
Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe	225	230	235
Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly	245	250	255
Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys			

260					265					270						
Lys	Leu	Ala	Tyr	Leu	Glu	Gln	Gln	Leu	Ser	Ser	Asn	Leu	Lys	Ala	Thr	
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Gln	Asn	Arg	Ile	Trp	Ser	Gly	Val	Thr	Lys	Asp	Val	Gly	Tyr	Leu	Arg	
290					295					300						
Arg	Met	Leu	Asn	Glu	Leu	Tyr	Ile	Leu	Lys	Val	Lys	Pro	Val	Tyr	Thr	
305					310					315					320	
Asp	Val	Asp	Ile	Ala	Tyr	Thr	Leu	Pro	Arg	Ser	Asn	Ser	Cys	Pro	Asp	
325					330					335						
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340					345					350						
Ala	Phe	Ser	Val	Cys	Ala	Asp	Met	Val	Gly	Ala	Gln	Arg	Glu	Ala	Gly	
355					360					365						
Met	Val	His	Ala	Asn	Ser	Asp	Thr	Asp	Leu	Thr	Lys	Leu	Asp	Arg	Glu	
370					375					380						
Lys	Thr	Phe	Glu	Thr	Ala	Glu	Ala	Tyr	His	Gln	Thr	Thr	Asp	Leu	Leu	
385					390					395					400	
Ala	Lys	Val	Val	Asn	Ala	Leu	Ala	Thr	Val	Lys	Pro	Pro	Pro	Ala	Glu	
405					410					415						
Gln	Glu	Asp	Ala	Ala	Leu	Tyr	Gly	Gly	Tyr	His	Gly	Phe	Ser	Asp	Ser	
420					425					430						
Gln	Ile	Leu	Ala	Ser	Glu	Trp	Ser	Phe	Ser	Thr	Val	Asn	Glu	Phe	Thr	
435					440					445						
Ser	Pro	Arg	Arg	Pro	Arg	Ala	Arg	Ala	Cys	Ser	Asp	Phe	Asn	Leu	Glu	
450					455					460						
Ala	Pro	Arg	Trp	Gln	Ser	Glu	Arg	Pro	Leu	Arg	Ser	Ser	His	Asn	Glu	
465					470					475					480	

Trp

<210> 38
 <211> 337
 <212> PRT

<213> Caenorhabditis elegans

<220>

<221> UNSURE

<222> (337)

<223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

<400> 38

Met	Ser	Asp	Gln	Leu	Phe	Val	Ala	Phe	Glu	Lys	Tyr	Phe	Leu	Thr	Ser
1				5					10					15	

Asn	Glu	Val	Lys	Lys	Asn	Ala	Ala	Thr	Glu	Thr	Trp	Thr	Phe	Ser	Ser
			20					25					30		

Ser	Ile	Phe	Phe	Ala	Val	Thr	Val	Val	Thr	Thr	Ile	Gly	Tyr	Gly	Asn
		35						40				45			

Pro	Val	Pro	Val	Thr	Asn	Ile	Gly	Arg	Ile	Trp	Cys	Ile	Leu	Phe	Ser
	50					55					60				

Leu	Leu	Gly	Ile	Pro	Leu	Thr	Leu	Val	Thr	Ile	Ala	Cys	Leu	Ala	Gly
65						70				75					80

Lys	Phe	Leu	Ser	Glu	His	Leu	Val	Trp	Leu	Tyr	Gly	Asn	Tyr	Leu	Lys
				85					90					95	

Leu	Lys	Tyr	Leu	Ile	Leu	Ser	Arg	His	Arg	Lys	Glu	Arg	Arg	Glu	His
			100					105						110	

Val	Cys	Glu	His	Cys	His	Ser	His	Gly	Met	Gly	His	Asp	Met	Asn	Ile
		115						120				125			

Glu	Glu	Lys	Arg	Ile	Pro	Ala	Phe	Leu	Val	Leu	Ala	Ile	Leu	Ile	Val
		130				135					140				

Tyr	Thr	Ala	Phe	Gly	Gly	Val	Leu	Met	Ser	Lys	Leu	Glu	Pro	Trp	Ser
145					150					155					160

Phe	Phe	Thr	Ser	Phe	Tyr	Trp	Ser	Phe	Ile	Thr	Met	Thr	Thr	Val	Gly
				165					170						175

Phe	Gly	Asp	Leu	Met	Pro	Arg	Arg	Asp	Gly	Tyr	Met	Tyr	Ile	Ile	Leu
			180					185					190		

Leu	Tyr	Ile	Ile	Leu	Gly	Lys	Phe	Ser	Met	Lys	Lys	Lys	Gln	Lys	Phe
		195						200				205			

Lys	Ile	Phe	Leu	Gly	Leu	Ala	Ile	Thr	Thr	Met	Cys	Ile	Asp	Leu	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

210	215	220
Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln		
225	230	235 240
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val		
245	250	255
Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser		
260	265	270
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile		
275	280	285
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr		
290	295	300
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln		
305	310	315 320
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys		
325	330	335

Xaa

<210> 39
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DEGENERATE
 PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>
 <221> variation
 <222> (2)
 <223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39
 tnggatwygg wgaywyt

17

<210> 40
 <211> 18
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DEGENERATE
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40

rtcwccrwah ccd aydgt

18

<210> 41

<211> 28

<212> DNA

<213> Homo sapiens

<400> 41

cgcaggcaga gccacaaaga gtacacag

28

<210> 42

<211> 26

<212> DNA

<213> Homo sapiens

<400> 42

ggagatcagc taggcacat atttgg

26

<210> 43

<211> 26

<212> DNA

<213> Homo sapiens

<400> 43

atgctgcatg cctcatgctt cccagc

26

<210> 44

<211> 20

<212> DNA

<213> Homo sapiens

<400> 44

ggttatttaa agagagggt

20

<210> 45

<211> 426

<212> PRT

<213> Homo sapiens

<400> 45

Met	Leu	Pro	Ser	Ala	Ser	Arg	Glu	Arg	Pro	Gly	Tyr	Arg	Ala	Gly	Val
1				5					10					15	
Ala	Ala	Pro	Asp	Leu	Leu	Asp	Pro	Lys	Ser	Ala	Ala	Gln	Asn	Ser	Lys
			20					25					30		
Pro	Arg	Leu	Ser	Phe	Ser	Thr	Lys	Pro	Thr	Val	Leu	Ala	Ser	Arg	Val
		35					40						45		
Glu	Ser	Asp	Thr	Thr	Ile	Asn	Val	Met	Lys	Trp	Lys	Thr	Val	Ser	Thr
	50					55					60				
Ile	Phe	Leu	Val	Val	Val	Leu	Tyr	Leu	Ile	Ile	Gly	Ala	Thr	Val	Phe
65						70				75					80
Lys	Ala	Leu	Glu	Gln	Pro	His	Glu	Ile	Ser	Gln	Arg	Thr	Thr	Ile	Val
				85					90					95	
Ile	Gln	Lys	Gln	Thr	Phe	Ile	Ser	Gln	His	Ser	Cys	Val	Asn	Ser	Thr
			100					105					110		
Glu	Leu	Asp	Glu	Leu	Ile	Gln	Gln	Ile	Val	Ala	Ala	Ile	Asn	Ala	Gly
		115					120						125		
Ile	Ile	Pro	Leu	Gly	Asn	Thr	Ser	Asn	Gln	Ile	Ser	His	Trp	Asp	Leu
	130					135					140				
Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly	Phe
145					150					155					160
Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile	Ile
				165					170					175	
Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	Gly	Val
		180						185					190		
Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val	Glu
		195					200					205			
Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	Ile	Ile
	210					215					220				
Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	Ala	Leu
225					230					235					240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val
325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr
340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu
355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu
370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu
385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly
405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
420 425

<210> 46

<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (35)

<223> N AT POSITION 35 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
 <221> unsure
 <222> (2057)
 <223> N AT POSITION 2057 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2067)
 <223> N AT POSITION 2067 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2111)
 <223> N AT POSITION 2111 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2120)
 <223> N AT POSITION 2120 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 46
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 cgtgcagctcggagcgcgcagcccgtctctgaataagaagttagtacaatggcgtgtttg 120
 taaaaaaaaagcttcaagtccgtctttttcaaaaaacattttgaatgctgc atgcctcatg 180
 cttcccagcgcctcgcgggagagaccggctatagagcagagtgggcggcacctgacttg 240
 ctggatccta aatctgcgcgc tcagaactccaaaccgaggctctcattttcacgaaaccc 300
 acagtgccttgcttcccgggtggagagtgacacgaccattaatgttatgaaatggaagacg 360
 gtctccacgataattcctgggtgttgctcttatctgatcatcgagaccacgtgttcaaaa 420
 gcattggagcagcctcatgagatttcacagaggaccacca ttgtgatcca gaagcaaaaa 480
 ttcatatccc aacattcctgtgtcaattcgcggagctggatgaactcat tcagcaaaaa 540
 gtggcagcaataaatgcagggattataccgttaggaaacacctccaatcaaatcagtcac 600
 tgggattttgggaagttccttcttctttgctggcactgttatacaacataggatttgga 660
 aacatctcacacgcacagaggcgcaaaaatattctgtatcatctatgccttactggga 720
 attcccctctttgggttttctcttggctgga gttggagatcagctaggcaccatatttgga 780
 aaaggaattgccaagtggagatacgtttattaagtggatgttagtca gaccaagatt 840
 cgcacatctcaacaatcatatttatactatttggtgtgtactctttgtggctctgcct 900
 gcgatcatat tcaaacacatagaaggctggagtgccttgacgcattttttttgtggtt 960
 atcactctaa caactattggatttggtgactacgttgacgtggatccga tattgaatat 1020
 ctggacttctataagcctgtcgtgtggttc tggatccttgtagggcttgcttactttgct 1080
 gctgtcctgagcatgattggagattggctcgagtgatctaaaaagacaaaagaagag 1140
 gtgggagagt tcagagcaca cgctgctgagtgacagccaacgtcacagcgaattcaaaa 1200
 gaaaccaggaggcgactgagtgtggagatttatgacaagt tccagcgggcacctccatc 1260
 aagcgggaagctctcggcagaactggctgga aaccacaatcaggagctgactccttgtag 1320

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aggaccctgt cagtgaacca cctgaccagc gagagggatg tcttgccctcc cttactgaag 1380
actgagagta tctatctgaa tggtttggcg ccacactgtg ctggtgaaga gattgctgtg 1440
attgagaaca tcaaatagcc ctctctttaa ataaccttag gcatagccat aggtgaggac 1500
ttctctatgc tctttatgac tgttgctggt agcatttttt aaattgtgca tgagctcaaa 1560
gggggaacaa aatagataca cccatcatgg tcatctatca tcaagagaat ttggaattct 1620
gagccagcac tttctttctg atgatgcttg ttgaacggcc cactttcttt gatgagtgga 1680
atgacaagca atgtctgatg cttttgtgtg cccagactgt tttcctctct ctttccctaa 1740
tgtgccataa ggccctcagaa tgaattgaga attgtttctg gtaacaatgt agctttgagg 1800
gatcagttct taacttttca gggctctacct aactgagcct agatatggac ctttatgga 1860
tgacaacaat tttttttttg taaatgacaa gaaattctta tgcagccttt tacctaagaa 1920
atttctgtca gtgccttata ttatgaagaa acagaacctc tctagctaata gtgtggtttc 1980
tccttccctg cccccacccc taggctcacc tctgcagtct tttacccag ttctccatt 2040
tgaataccat accttgntgg aaacagngtg taaaatgact gaagtgatga tgccgaagat 2100
gaaatagatg ncaaattagn tggacattga 2130

```

```

<210> 47
<211> 27
<212> DNA
<213> Homo sapiens

```

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<400> 47
aaaagatcta aaatgcttcc cagcgcc 27

```

```

<210> 48
<211> 27
<212> DNA
<213> Homo sapiens

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```

<400> 48
aaagtcgacc tatttgatgt tctcaat 27

```

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<210> 49
<211> 27
<212> DNA
<213> Homo sapiens

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```

<400> 49
aaaaagctta aaatgcttcc cagcgcc 27

```

```

<210> 50
<211> 27
<212> DNA
<213> Homo sapiens

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<400> 50
aaatctagac tatttgatgt tctcaat

27

<210> 51
<211> 534
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (262)
<223> N AT POSITION 262 INDICATES UNDETERMINED
NUCLEOTIDE

<400> 51
aacaaaaaacc ttttttgttt tgaatggcct agagagggta agggatcccc tgacgaacag 60
gagcagagcc agctagaacc tgggcctggc cagttcaagg ccaccagagg gcagccttct 120
gcggaaggca gtattggggg aggcagggac cccagcagac atggcactca gagctctcac 180
tgtccactga ctctctcttc tccaggttat ggccacatgg cccactatc gccaggcgga 240
aaggccttct gcatggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300
accctgcgcc attgcctgct gcctgtgctc agccgcccac gtgcctgggt agcgggtccac 360
tggcagctgt caccggccag ggctgcgctg ctgcaggcag ttgcactggg actgctggtg 420
gccagcagct ttgtgctgct gccagcgctg gtgctgtggg gccttcaggg cgactgcagc 480
ctgctggggg ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52
<211> 956
<212> DNA
<213> Mus musculus

<400> 52
atgatacgat ttaatacgac tcactatagg gaatttgccc ctcgaggcca agaattcggc 60
acgaggagaa tgtgcgcacg ttggctctca tcgtgtgcac cttcacctac ctgctggtgg 120
gcgccgcggg gttcgacgca ctggagtcgg agccggagat gatcgagcgg cagcggctgg 180
agctgcggca gctggagctg cgggcgcgct acaacctcag cgagggcggc tacgaggagc 240
tggagcgcgt cgtgctgcgc ctcaagccgc acaaggccgg cgtgcagtgg cgcttcgccg 300
gtcctttcta cttcgccatc accgtcatca ccaccatcgg ctatgggtcat gcggcgccca 360
gcacggacgg aggcaagggt ttctgcatgt tctacgcgct gctgggcatc ccgctcacac 420
tagtcatgtt ccagagcctg ggtgaacgca tcaacacctc cgtgaggtac ctgctgcacc 480
gtgccaaagag ggggctgggc atgcggcacg ccgaagtgtc catggccaac atggtgctca 540
tcggtttctg gtcgtgcacg agcacgctgt gcatcggcgc agctgccttc tcctactacg 600
agcgtgggac tttcttcag gcctattact actgcttcat caccctcacc accatcggct 660
tcggcgacta tgtggcgctg cagaaggacc aggcgctgca gacgcagccg cagtatgtgg 720
cttcagcttc gtgtacatcc tcacgggctc acggtcatcg gcgcttcctc aacctcgtgg 780
tgctgcgatt catgaccatg aacgccgagg acgagaagcg tgatgcggag caccgcgccc 840
tgctcacgca caacggccag gctgtcggcc tgggtggcct gagctgcctg agcggtagcc 900

tgggcgacgg cgtgcgtccc cgcgaccag tcacatgcgc tgcggccgca agctta 956

<210> 53

<211> 1055

<212> DNA

<213> Mus musculus

<220>

<221> unsure

<222> (247)

<223> N AT POSITION 247 INDICATES UNDETERMINED
NUCLEOTIDE

<220>

<221> unsure

<222> (593)

<223> N AT POSITION 593 INDICATES UNDETERMINED
NUCLEOTIDE

<220>

<221> unsure

<222> (952)

<223> N AT POSITION 952 INDICATES UNDETERMINED
NUCLEOTIDE

<400> 53

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ctgaaacat gggcccgata cctgctcctg cttatggccc acctgctggc catgggcctt 60
ggggctgtgg tgcttcaggc cctggagggc cctccagctc gccacctcca ggcccaggtc 120
caggctgaac tggctagctt ccaggcagag cacagggcct gcttgccacc tgaggccctg 180
gaggagctgc taggtgcggt cctgagagca caggcccatg gagtttccag cctgggcaac 240
agctcanaga caagcaactg ggatctgccc tcagctctgc tgttcactgc cagcatcctc 300
accaccaccg gttatggcca catggcccca ctctcctcag gtggaaaggc cttctgtgtg 360
gtctatgcag cccttgggct gccagcctct ctagcacttg tggctgccct gcgccactgc 420
ttgctgcctg tgttcagtcg cccaggtgac tgggtagcca ttcgctggca gctggcacca 480
gtcaggctg ctctgctaca ggcagcagga ctgggcctcc tgggtggcctg tgtcttcatg 540
ctgctgccag cactggtgct gtggggtgta cagggtgact ggcagcctgc tanaaccatc 600
tacttctgtt tcggctcact cagcacgatc ggcctaggag acttgctgcc tgcccatgga 660
cgtggcctgc accagccat ttaccacctt gggcagtttg cacttcttgg ttacttgctc 720
ctggggctcc tggccatgtt gttagcagta gagaccttct cagagctgcc tcaggctccg 780
gccatggtga aattcttttg gccagtggc tctagaaccg atgaagatca agatggcatc 840
ctaggccaag atgagctggc tctgagcact gtgctgcctg acgccccagt cttgggacca 900
accacccag cctgagcggg aggcaccaag gagtgcttga agaacatagc angaagggtt 960
atgggaatga atatgtcatg ggataatgtt aattttaaaa attaaatggg ctgcttagca 1020
tgcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1055
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<210> 54

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (88)

<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 54

Asn	Lys	Asn	Leu	Phe	Cys	Phe	Glu	Trp	Pro	Arg	Glu	Gly	Lys	Gly	Ser
1				5					10					15	

Pro	Asp	Glu	Gln	Glu	Gln	Ser	Gln	Leu	Glu	Pro	Gly	Pro	Gly	Gln	Phe
		20						25					30		

Lys	Ala	Thr	Arg	Gly	Gln	Pro	Ser	Ala	Glu	Gly	Ser	Ile	Gly	Val	Gly
		35					40					45			

Arg	Asp	Pro	Ser	Arg	His	Gly	Thr	Gln	Ser	Ser	His	Cys	Pro	Leu	Thr
	50					55					60				

Leu	Ser	Ser	Pro	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser	Pro	Gly	Gly
65					70					75					80

Lys	Ala	Phe	Cys	Met	Val	Leu	Xaa	Ala	Leu	Gly	Leu	Pro	Ala	Ser	Leu
			85						90					95	

Ala	Leu	Val	Ala	Thr	Leu	Arg	His	Cys	Leu	Leu	Pro	Val	Leu	Ser	Arg
		100						105					110		

Pro	Arg	Ala	Trp	Val	Ala	Val	His	Trp	Gln	Leu	Ser	Pro	Ala	Arg	Ala
		115					120					125			

Ala	Leu	Leu	Gln	Ala	Val	Ala	Leu	Gly	Leu	Leu	Val	Ala	Ser	Ser	Phe
	130						135				140				

Val	Leu	Leu	Pro	Ala	Leu	Val	Leu	Trp	Gly	Leu	Gln	Gly	Asp	Cys	Ser
145					150					155					160

Leu	Leu	Gly	Ala	Val	Tyr	Phe	Cys	Phe	Ser	Ser	Leu	Ser	Thr	Ile	Gly
			165						170					175	

Leu Gly

<210> 55

<211> 309

<212> PRT

<213> Mus musculus

<400> 55

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala

Ser	Ser	Xaa	Thr	Ser	Asn	Trp	Asp	Leu	Pro	Ser	Ala	Leu	Leu	Phe	Thr	85	90	95	
Ala	Ser	Ile	Leu	Thr	Thr	Thr	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser	100	105	110	
Ser	Gly	Gly	Lys	Ala	Phe	Cys	Val	Val	Tyr	Ala	Ala	Leu	Gly	Leu	Pro	115	120	125	
Ala	Ser	Leu	Ala	Leu	Val	Ala	Ala	Leu	Arg	His	Cys	Leu	Leu	Pro	Val	130	135	140	
Phe	Ser	Arg	Pro	Gly	Asp	Trp	Val	Ala	Ile	Arg	Trp	Gln	Leu	Ala	Pro	145	150	155	160
Ala	Gln	Ala	Ala	Leu	Leu	Gln	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Val	Ala	165	170	175	
Cys	Val	Phe	Met	Leu	Leu	Pro	Ala	Leu	Val	Leu	Trp	Gly	Val	Gln	Gly	180	185	190	
Asp	Trp	Gln	Pro	Ala	Xaa	Thr	Ile	Tyr	Phe	Cys	Phe	Gly	Ser	Leu	Ser	195	200	205	
Thr	Ile	Gly	Leu	Gly	Asp	Leu	Leu	Pro	Ala	His	Gly	Arg	Gly	Leu	His	210	215	220	
Pro	Ala	Ile	Tyr	His	Leu	Gly	Gln	Phe	Ala	Leu	Leu	Gly	Tyr	Leu	Leu	225	230	235	240
Leu	Gly	Leu	Leu	Ala	Met	Leu	Leu	Ala	Val	Glu	Thr	Phe	Ser	Glu	Leu	245	250	255	
Pro	Gln	Val	Arg	Ala	Met	Val	Lys	Phe	Phe	Gly	Pro	Ser	Gly	Ser	Arg	260	265	270	
Thr	Asp	Glu	Asp	Gln	Asp	Gly	Ile	Leu	Gly	Gln	Asp	Glu	Leu	Ala	Leu	275	280	285	
Ser	Thr	Val	Leu	Pro	Asp	Ala	Pro	Val	Leu	Gly	Pro	Thr	Thr	Pro	Ala	290	295	300	

<210> 57

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1)..(9)
<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT
POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8
IS Y, F, V, I, M, OR L

<220>
<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<400> 57
Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
1 5

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>
<221> VARIANT
<222> (1)..(8)
<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I,
V, L, F, OR Y

<400> 58
Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa
1 5

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: POTASSIUM ION

CHANNEL SEQUENCE

<400> 59

Tyr Ala Leu Leu Gly Ile Pro

1

5

<210> 60

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (6)

<223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60

Tyr Ala Leu Leu Gly Xaa Pro

1

5

<210> 61

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (88)

<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser

1

5

10

15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe

20

25

30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly

35

40

45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr

50

55

60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
165 170 175

Leu Gly

<210> 62

<211> 309

<212> PRT

<213> Mus musculus

<400> 62

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala

<213> Caenorhabditis elegans

<400> 63

Met	Val	Ile	Ile	Asn	Arg	Ser	Asn	Thr	Tyr	Ala	Val	Glu	Gln	Glu	Ala
1				5				10					15		
Phe	Pro	Arg	Asp	Lys	Tyr	Asn	Ile	Val	Tyr	Trp	Leu	Val	Ile	Leu	Val
			20					25					30		
Gly	Phe	Gly	Val	Leu	Leu	Pro	Trp	Asn	Met	Phe	Ile	Thr	Ile	Ala	Pro
		35					40					45			
Glu	Tyr	Tyr	Val	Asn	Tyr	Trp	Phe	Lys	Pro	Asp	Gly	Val	Glu	Thr	Trp
	50					55					60				
Tyr	Ser	Lys	Glu	Phe	Met	Gly	Ser	Leu	Thr	Ile	Gly	Ser	Gln	Leu	Pro
65					70					75					80
Asn	Ala	Ser	Ile	Asn	Val	Phe	Asn	Leu	Phe	Leu	Ile	Ile	Ala	Gly	Pro
				85					90					95	
Leu	Ile	Tyr	Arg	Val	Phe	Ala	Pro	Val	Cys	Phe	Asn	Ile	Val	Asn	Leu
			100					105					110		
Thr	Ile	Ile	Leu	Ile	Leu	Val	Ile	Val	Leu	Glu	Pro	Thr	Glu	Asp	Ser
		115					120						125		
Met	Ser	Trp	Phe	Phe	Trp	Val	Thr	Leu	Gly	Met	Ala	Thr	Ser	Ile	Asn
	130					135					140				
Phe	Ser	Asn	Gly	Leu	Tyr	Glu	Asn	Ser	Val	Tyr	Gly	Val	Gly	Gly	Asp
145					150					155					160
Phe	Pro	His	Thr	Tyr	Ile	Gly	Ala	Leu	Leu	Ile	Gly	Asn	Asn	Ile	Cys
				165					170					175	
Gly	Leu	Leu	Ile	Thr	Val	Val	Lys	Ile	Gly	Val	Thr	Tyr	Phe	Leu	Asn
			180					185					190		
Asp	Glu	Pro	Lys	Leu	Val	Ala	Ile	Val	Tyr	Phe	Gly	Ile	Ser	Leu	Val
		195						200				205			
Ile	Leu	Leu	Val	Cys	Ala	Ile	Ala	Leu	Phe	Phe	Ile	Thr	Lys	Gln	Asp
	210						215					220			
Phe	Tyr	His	Tyr	His	His	Gln	Lys	Gly	Met	Glu	Ile	Arg	Glu	Lys	Ala
225					230					235					240

Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn
 245 250 255
 Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu
 260 265 270
 Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly
 275 280 285
 Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu
 290 295 300
 Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val
 305 310 315 320
 Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile
 325 330 335
 Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn Tyr Arg
 340 345 350
 Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe
 355 360 365
 Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala
 370 375 380
 Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
 385 390 395 400
 Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr
 405 410 415
 Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser
 420 425 430
 Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
 CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,
L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro
1 5

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<400> 65

Thr Trp Thr Phe
1

<210> 66

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 66

Gly Tyr Gly Asn
1

<210> 67

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 67

Gly Phe Gly Asp

